REMARKS

Responsive to the Notfification to Comply with Sequence Listing Requirements, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.821(f) and 1.821(g).

I hereby state, in accordance with 37 C.F.R. §1.821(f), that the content of the paper copy sequence listing as filed and the attached computer readable copy of the sequence listing are believed to be the same.

I hereby also state, in accordance with 37 C.F.R. §1.821(g), that the submission is not believed to include new matter.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that

organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The paragraph beginning at line 3 of page 33 has been amended as follows:

TABLE 3a
Predicted human Uroplakin Ib, II and III peptides that bind to HLA-A2

Peptide	Start Position	Sequence	SEQ ID NO:
Uroplakin Ib/B1	239	AILCWTFWV	50
Uroplakin Ib/B2	92	FILMFIVYA	51
Uroplakin Ib/B3	29	LTASFIFFV	52
Uroplakin Ib/B4	154	MLQDICCGV	53
Uroplakin Ib/B5	240	ILCWTFWVL	54
Uroplakin Ib/B6	89	KILLAYFIL	55
Uroplakin Ib/B7	44	FVGICLFCL	56
Uroplakin II/1	161	VLLSVAMFL	57
Uroplakin II/2	162	LLSVAMFLL	58
Uroplakin III 3.1	214	IIGSIPFFL	59
Uroplakin III 3.2	139	IINAYLVFV	60
Uroplakin III/3.3	221	FLLVGFAGA	61
Uroplakin III 3.4	20	NLQFQLASV	62
Uroplakin III/3.5	47	CMFDFKEAL	63
Uroplakin III/3.6	62	YLYVLVDSA	64
Tyrosinase	368	YMDGTMSQV	65

Table 3a shows the sequences of the peptides tested in single letter amino acid code and their starting position in the intact protein (according to NCBI accession nos. 3298345 (peptides 3.1-3.6), 3483011 (peptides 8 and 9), and 3721858 (peptides B1-B7).

The paragraph beginning at line 21 of page 43 has been amended as follows:

TABLE 9

Predicted human Cripto-1 derived peptides that bind to HLA-A2

Peptide	Start Position	Sequence	SEQ ID NO:
Cripto-1 C1	5	[illegible]	66
Cripto-1 C2	151	[illegible]	67
Cripto-1 C3	145	[illegible]	68
Cripto-1 C4	89	[illegible]	69
Cripto-1 C5	43	[illegible]	70
Cripto-1 C6	123	[illegible]	71
Cripto-1 C7	83	[illegible]	72
Cripto-1 C8	176	[illegible]	73
Cripto-1 C9	23	[illegible]	74
Cripto-1 C10	5	[illegible]	75
Cripto-1 C11	83	[illegible]	76
Cripto-1 C12	176	[illegible]	77

Table 9 shows the sequences of the peptides tested in single letter amino acid code and their starting position in the intact protein according to NCBI accession nos. 117473 (C1-C9) and 321120 (C10-C12).